NCBI **Blast 2 Sequences results**
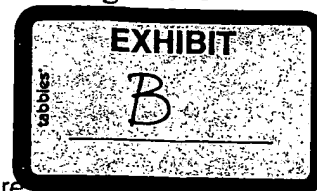
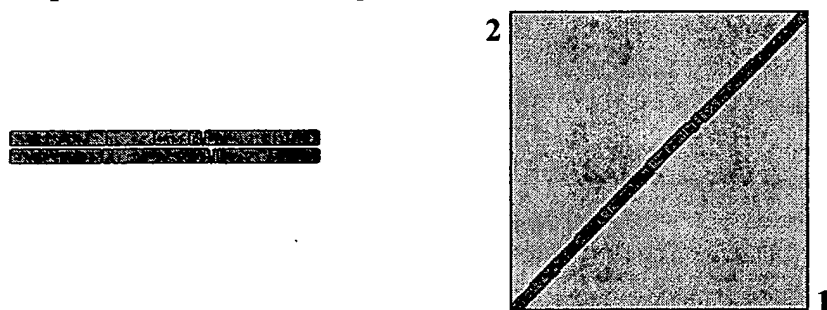PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Align

Sequence 1 lcl|seq_1 **Length** 862 (1 .. 862)

Sequence 2 lcl|seq_2 **Length** 859 (1 .. 859)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 1202 bits (3110), Expect = 0.0
Identities = 637/869 (73%), Positives = 704/869 (80%), Gaps = 17/869 (1%)
```



```
Query: 1    MERAESSSTEPAKAIKPIDRKSVHQICSGQVVLSLSTAVKELVENSLDAGATNIDLKLKD 60
            ME+ E  STE AKAIKPID KSVHQICSGQV+LSLSTAVKEL+ENS+DAGAT IDL+LKD
Sbjct: 1    MEQTEGVSTECAKAIKPIDGKSVHQICSGQVILSLSTAVKELIENSVDAGATTIDLRLKD 60

Query: 61   YGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120
            YGVDLIEVSDNGCGVEEENFEGL LKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV
Sbjct: 61   YGVDLIEVSDNGCGVEEENFEGLALKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDV 120

Query: 121  TISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQRNIKKE 180
            TISTCH SA VGTRL+FDHNGKI QKTPYPRP+GTTVSVQ LF TLPVR+KEFQRNIKKE
Sbjct: 121  TISTCHGSASVGTRLVFDHNGKITQKTPYPRPKGTTVSVQHLFYTLPVRYKEFQRNIKKE 180

Query: 181  YAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSIKENIGSVFGQKQLQSLI 240
            Y+KMVQVL AYCIISAG+RVSCTNQLGQGKR  VVCT G+   +KENIGSVFGQKQLQSLI
Sbjct: 181  YSKMVQVLQAYCIISAGVRVSCTNQLGQGKRHAVVCTSGTSGMKENIGSVFGQKQLQSLI 240

Query: 241  PFVQLPPSDSVCEEYGLSCSDALHNLF--YISGFISQCTHGVGRSSTDRQFFFINRRPCD 298
            PFVQLPPSD+VCEEYGLS S   H F + + F S T   G   T   F   R P
Sbjct: 241  PFVQLPPSDAVCEEYGLSTSGR-HKTFSTFRASFHSARTAPGGVQQTG-SFSSSIRGPVT 298

Query: 299  PAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358
               +  L    YHMYNRHQYPFVVLN+SVDSECVDINVTPDKRQILLQEEKLLLAVLKTS
Sbjct: 299  QQRSLSLSMRFYHMYNRHQYPFVVLNVSVDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358

Query: 359  LIGMFDSDVNKLNVSQQPLLDVEGNLIKMHAADLEKPMVEKQDQSPSLR-TGEEKKDVSI 417
            LIGMFDSD NKLNV+QQPLLDVEGNL+K+H A+LEKP+ KQD SPSL+ T +EK+  SI
```

```
Sbjct: 359 LIGMFDSDANKLNVNQQPLLDVEGNLVKLHTAELEKPVPGKQDNSPSLKSTADEKRVASI 418

Query: 418 SRLREAFSLRHTTENKPHSPKTPEPRRSPLGQKRGMLSSSTSGAISDKGVLRPQKEAVSS 477
           SRLREAFSL  T E K    P+T E  RS   +KRG+LSS  S  IS +G+   Q + VS
Sbjct: 419 SRLREAFSLHPTKEIKSRGPETAELTRSFPSEKRGVLSSYPSDVISYRGLRGSQDKLVSP 478

Query: 478 SHGPSDPTDRAEVEKDSGHGSTSVDSEG-FSIPDTGSHCSSEYAASSPGDRGSQEHVDSQ 536
           +  P D  DR ++EKDSG  STS  SE  FS P+  S  SS+Y  SS  DR SQE ++
Sbjct: 479 TDSPGDCMDREKIEKDSGLSSTSAGSEEEFSTPEVASSFSSDYNVSSLEDRPSQETINCG 538

Query: 537 E---KAPETDDSFSDVDCHSNQEDTGCKFRVLPQPTNLATPNTKRFKKEEILSSSDICQK 593
           +   + P T  S          ED G + + LP    L+  N KRFK EE  S+ +I Q+
Sbjct: 539 DLDCRPPGTGQSLKP-------EDHGYQCKALPL-ARLSPTNAKRFKTEERPSNVNISQR 590

Query: 594 LVNTQDMSASQVDVAVKINKKVVPLDFSMSSLAKRIKQLHHEAQQSEGEQNYRKFRAKIC 653
           L   Q  SA++VDVA+K+NK++V L+FS+SSLAKR+KQL H   Q++ E +YRKFRAKIC
Sbjct: 591 LPGPQSTSAAEVDVAIKMNKRIVLLEFSLSSLAKRMKQLQHLKAQNKHELSYRKFRAKIC 650

Query: 654 PGENQAAEDELRKEISKTMFAEMEIIGQFNLGFIITKLNEDIFIVDQHATDEKYNFEMLQ 713
           PGENQAAEDELRKEISK+MFAEMEI+GQFNLGFI+TKL ED+F+VDQHA DEKYNFEMLQ
Sbjct: 651 PGENQAAEDELRKEISKSMFAEMEILGQFNLGFIVTKLKEDLFLVDQHAADEKYNFEMLQ 710

Query: 714 QHTVLQGQRLIAPQTLNLTAVNEAVLIENLEIFRKNGFDFVIDENAPVTERAKLISLPTS 773
           QHTVLQ QRLI PQTLNLTAVNEAVLIENLEIFRKNGFDFVIDE+APVTERAKLISLPTS
Sbjct: 711 QHTVLQAQRLITPQTLNLTAVNEAVLIENLEIFRKNGFDFVIDEDAPVTERAKLISLPTS 770

Query: 774 KNWTFGPQDVDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMIGTALNTSEMKKLITH 833
           KNWTFGPQD+DELIFMLSDSPGVMCRPSRV+QMFASRACRKSVMIGTALN SEMKKLITH
Sbjct: 771 KNWTFGPQDIDELIFMLSDSPGVMCRPSRVRQMFASRACRKSVMIGTALNASEMKKLITH 830

Query: 834 MGEMDHPWNCPHGRPTMRHIANLGVISQN 862
           MGEMDHPWNCPHGRPTMRH+ANL VISQN
Sbjct: 831 MGEMDHPWNCPHGRPTMRHVANLDVISQN 859
```

```
CPU time:      0.17 user secs.      0.04 sys. secs      0.21 total secs.

Lambda      K        H
   0.315    0.131     0.371

Gapped
Lambda      K        H
   0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 6158
Number of Sequences: 0
Number of extensions: 502
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 859
length of database: 461,760,005
effective HSP length: 136
effective length of query: 723
effective length of database: 461,759,869
```

```
effective search space: 333852385287
effective search space used: 333852385287
T: 9
A: 40
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 79 (35.0 bits)
```